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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/941,193A

DATE: 07/23/2002 06
TIME: 13:04:51

Input Set : A:\Seqsub2.app
Output Set: N:\CRF3\07232002\I941193A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: BROW, MARY ANN D.
7 LYAMICHEV, VICTOR I.
8 OLIVE, DAVID M.
10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
11 PATHOGENS
13 (iii) NUMBER OF SEQUENCES: 165
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: MEDLEN & CARROLL
17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
18 (C) CITY: SAN FRANCISCO
19 (D) STATE: CALIFORNIA
20 (E) COUNTRY: UNITED STATES OF AMERICA
21 (F) ZIP: 94104
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/941,193A
C--> 31 (B) FILING DATE: 28-Aug-2001
32 (C) CLASSIFICATION:
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: CARROLL, PETER G.
36 (B) REGISTRATION NUMBER: 32,837
37 (C) REFERENCE/DOCKET NUMBER: FORS-01756
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (415) 705-8410
41 (B) TELEFAX: (415) 397-8338
44 (2) INFORMATION FOR SEQ ID NO: 1:
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 2506 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear
52 (ii) MOLECULE TYPE: DNA (genomic)
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58 ATGAGGGGGA TGCTGCCCT CTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC 60
60 CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG 120
62 GTGCAGGCAG 62 GTGCAGGCAG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC 180
64 GCGGTGATCG TGGTCTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG 240

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|-----|--|-------------|------------|------------|-------------|-------------|------|
| 66 | TACAAGGCGG | CCCGGGCCCC | CACGCCGGAG | GACTTCCCC | GGCAACTCGC | CCTCATCAAG | 300 |
| 68 | GAGCTGGTGG | ACCTCCTGGG | GCTGGCGCGC | CTCGAGGTCC | CGGGCTACGA | GGCGGACGAC | 360 |
| 70 | GTCCTGGCCA | GCCTGGCAA | GAAGGCGGAA | AAGGAGGGCT | ACGAGGTCCG | CATCCTCACC | 420 |
| 72 | GCCGACAAAG | ACCTTACCA | GCTCCTTCC | GACCGCATCC | ACGTCCCTCA | CCCCGAGGGG | 480 |
| 74 | TACCTCATCA | CCCCGGCTG | GCTTGGGAA | AAGTACGGCC | TGAGGCCCCA | CCAGTGGGCC | 540 |
| 76 | GAECTACCGG | CCCTGACCGG | GGACGAGTCC | GACAACCTTC | CCGGGGTCAA | GGGCATCGGG | 600 |
| 78 | GAGAACAGCG | CGAGGAAGCT | TCTGGAGGAG | TGGGGAGCC | TGGAAGCCCT | CCTCAAGAAC | 660 |
| 80 | CTGGACCGGC | TGAAGCCC | CATCCGGAG | AAGATCCTGG | CCCACATGGA | CGATCTGAAG | 720 |
| 82 | CTCTCCTGGG | ACCTGGCAA | GGTGC | GACCTGCCCC | TGGAGGTGGA | CTTCGCCAAA | 780 |
| 84 | AGGCGGGAGC | CCGACCGGG | GAGGCTTAGG | GCTTCTG | AGAGGCTTGA | GTTTGGCAGC | 840 |
| 86 | CTCCTCCACG | AGTTCGGC | TCTGGAAAGC | CCCAAGGCC | TGGAGGAGGC | CCCCCTGGCCC | 900 |
| 88 | CCGCCGGAAG | GGGCCTCGT | GGGCTTTGTG | CTTTC | AGGAGCCCAT | GTGGGCCGAT | 960 |
| 90 | CTTCTGGCCC | TGGCCGCC | CAGGGGGGGC | CGGGTCCACC | GGGCCCCCGA | GCCTTATAAA | 1020 |
| 92 | GCCCTCAGGG | ACCTGAAGGA | GGCGCGGGGG | CTTCTCGCCA | AAGACCTGAG | CGTTCTGCC | 1080 |
| 94 | CTGAGGAAG | GCCTTGCCT | CCCGCCCGC | GACGACCCCA | TGCTCCTCGC | CTACCTCCTG | 1140 |
| 96 | GACCCCTCCA | ACACCACCCC | CGAGGGGGTG | GCCC | ACGGCGGGGA | GTGGACGGAG | 1200 |
| 98 | GAGGCGGGGG | AGCGGGCCG | CCTTCCGAG | AGGCTT | CCAACCTGTG | GGGGAGGCTT | 1260 |
| 100 | GAGGGGGAGG | AGAGGCTCCT | TTGGCTTAC | CGGGAGGTGG | AGAGGCCCT | TTCCGCTGTC | 1320 |
| 102 | CTGGCCCACA | TGGAGGCCAC | GGGGGTGCGC | CTGGACGTGG | CCTATCTCAG | GGCCTTGTCC | 1380 |
| 104 | CTGGAGGTGG | CCGAGGAGAT | CGCCCGCCTC | GAGGCCGAGG | TCTTCCG | GGCCGGCCAC | 1440 |
| 106 | CCCTTCAACC | TCAACTCCC | GGACCAGCTG | GAAAGGGTCC | TCTTGACGA | GCTAGGGCTT | 1500 |
| 108 | CCGCCATCG | GCAAGACGG | GAAGACCGGC | AAGCGCTCA | CCAGCGCCG | CGTCTGGAG | 1560 |
| 110 | GCCCTCCGCG | AGGCCACCC | CATCGTGGAG | AAGATCCTGC | AGTACCGGGA | GCTCACCAAG | 1620 |
| 112 | CTGAAGAGCA | CCTACATTGA | CCCCTGCG | GACCTCATCC | ACCC | GGCCGCCTC | 1680 |
| 114 | CACACCCGCT | TCAACCAGAC | GGCCACGGCC | ACGGCAGGC | TAAGTAGCTC | CGATCCAAAC | 1740 |
| 116 | CTCCAGAAC | TCCCCGTCCG | CACCCCGCTT | GGGCAGAGGA | TCCGCCGGC | CTTCATCGCC | 1800 |
| 118 | GAGGAGGGGT | GGCTATTGGT | GGCCCTGGAC | TATAGCCAGA | TAGAGCTCAG | GGTGTG | 1860 |
| 120 | CACCTCTCG | GCGACGAGAA | CCTGATCCGG | GTCTTCCAGG | AGGGGCGGGGA | CATCCACACG | 1920 |
| 122 | GAGACCGCCA | GCTGGATGTT | CGCGTCCCC | CGGGAGGCCG | TGGACCC | GATGCGCCGG | 1980 |
| 124 | GCGGCCAAGA | CCATCAACTT | CGGGGTCTC | TACGGCATGT | CGGCC | ACCGC | 2040 |
| 126 | GAGCTAGCCA | TCCCTTACGA | GGAGGCCAG | GCCTTCATTG | AGCGCTACTT | TCAGAGCTTC | 2100 |
| 128 | CCCAAGGTGC | GGGCCTGGAT | TGAGAAGACC | CTGGAGGAGG | GCAGGAGGCCG | GGGGTACGTG | 2160 |
| 130 | GAGACCCCTC | TCGGCCGCCG | CCGCTACGTG | CCAGACCTAG | AGGCCCGGGT | GAAGAGCGTG | 2220 |
| 132 | CGGGAGGCCG | CCGAGCGCAT | GGCCTCAAC | ATGCCGTCC | AGGGCACCGC | CGCCGACCTC | 2280 |
| 134 | ATGAAGCTGG | CTATGGTGA | GCTTCCCC | AGGCTGGAGG | AAATGGGGC | CAGGATGCTC | 2340 |
| 136 | CTTCAGGTCC | ACGACGAGCT | GTCCTCGAG | GCCCCAAAAG | AGAGGGCGGA | GGCCGTGCC | 2400 |
| 138 | CGGCTGGCCA | AGGAGGTCA | GGAGGGGGTG | TATCCCCTGG | CCGTGCC | GGAGGTGGAG | 2460 |
| 140 | GTGGGGATAG | GGGAGGACTG | GCTCTCCGCC | AAGGAGTGAT | ACCACC | | 2506 |
| 142 | (2) INFORMATION FOR SEQ ID NO: 2: | | | | | | |
| 144 | (i) SEQUENCE CHARACTERISTICS: | | | | | | |
| 145 | (A) LENGTH: 2496 base pairs | | | | | | |
| 146 | (B) TYPE: nucleic acid | | | | | | |
| 147 | (C) STRANDEDNESS: double | | | | | | |
| 148 | (D) TOPOLOGY: linear | | | | | | |
| 150 | (ii) MOLECULE TYPE: DNA (genomic) | | | | | | |
| 154 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: | | | | | | |
| 156 | ATGGCGATGC | TTCCCCCTCTT | TGAGCCAAA | GGCCCGTGC | TCCTGGTGA | CGGCCACCAC | 60 |
| 158 | CTGGCCTACC | GCACCTTCTT | TGCCCTCAAG | GGCCTCACCA | CCAGCGCGG | CGAACCCGTT | 120 |
| 160 | CAGGCGGTCT | ACGGCTTC | CAAAGCCTC | CTCAAGGCC | TGAAGGAGGA | CGGGGACGTG | 180 |

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|-----|--|-------------|-------------|-------------|-------------|------------|------|
| 162 | GTGGTGGTGG | TCTTGACGC | CAAGGCCCCC | TCCTTCCGCC | ACGAGGCCTA | CGAGGCCTAC | 240 |
| 164 | AAGGCAGGCC | GGGCCAC | CCCAGGAGAC | TTTCCCCGGC | AGCTGGCCCT | CATCAAGGAG | 300 |
| 166 | TTGGTGGACC | TCCTAGGCCT | TGTGGCGCTG | GAGGTTCCCG | GCTTGAGGC | GGACGACGTG | 360 |
| 168 | CTGGCCACCC | TGGCCAAGCG | GGCGGAAAAG | GAGGGGTACG | AGGTGCGCAT | CCTCACTGCC | 420 |
| 170 | GACCAGCGACC | TCTACCAGCT | CCTTCGGAG | CGCATCGCCA | TCCTCCACCC | TGAGGGGTAC | 480 |
| 172 | CTGATCACCC | CGGCGTGGCT | TTACGAGAAAG | TACGGCCTGC | GCCCGGAGCA | GTGGGTGGAC | 540 |
| 174 | TACCGGGCCC | TGGCGGGGGA | CCCCTCGGAT | AACATCCCCG | GGGTGAAGGG | CATCGGGGAG | 600 |
| 176 | AAGACCGCCC | AGAGGCTCAT | CCGCGAGTGG | GGGAGCCTGG | AAAACCTCTT | CCAGCACCTG | 660 |
| 178 | GACCAGGTGA | AGCCCTCCTT | GCAGGAGAAAG | CTCCAGGCGG | GCATGGAGGC | CCTGGCCCTT | 720 |
| 180 | TCCCAGGAAGC | TTTCCCAGGT | GCACACTGAC | CTGCCCCCTGG | AGGTGGACTT | CGGGAGGCAC | 780 |
| 182 | CGCACACCCA | ACCTGGAGGG | TCTGCGGGCT | TTTTGGAGC | GGTTGGAGTT | TGGAAGCCTC | 840 |
| 184 | CTCCACGAGT | TCGGCCTCCT | GGAGGGGCCG | AAGGCGGCAG | AGGAGGCC | CTGGCCCCCT | 900 |
| 186 | CGGGAAGGGG | CTTTTTGGG | CTTTTCCTT | TCCCGTCCCG | AGCCCATGTG | GGCCGAGCTT | 960 |
| 188 | CTGGCCCTGG | CTGGGGCGTG | GGAGGGGCCG | CTCCATCGGG | CACAAGACCC | CCTTAGGGGC | 1020 |
| 190 | CTGAGGGACC | TTAAGGGGGT | GCAGGGAAATC | CTGGCCAAGG | ACCTGGCGGT | TTTGGCCCTG | 1080 |
| 192 | CGGGAGGGCC | TGGACCTCTT | CCCAGAGGAC | GACCCCATGC | TCCTGGCCTA | CCTTCTGGAC | 1140 |
| 194 | CCCTCCAACA | CCACCCCTGA | GGGGGTGGCC | CGCGCTTACG | GGGGGGAGTG | GACGGAGGAT | 1200 |
| 196 | GGGGGGGAGA | GGGCCCTCCT | GGCCGAGCGC | CTCTTCCAGA | CCCTAAAGGA | GGCCCTTAAG | 1260 |
| 198 | GGAGAAGAAC | GCCTGCTTTG | GCTTACGAG | GAGGTGGAGA | AGCCGCTTTC | CGGGGTGTTG | 1320 |
| 200 | GCCCAGGATGG | AGGCCACGGG | GGTCCGGCTG | GACGTGGCCT | ACCTCCAGGC | CCTCTCCCTG | 1380 |
| 202 | GAGGTGGAGG | CGGAGGTGCG | CCAGCTGGAG | GAGGAGGTCT | TCCGCCTGGC | CGGCCACCC | 1440 |
| 204 | TTCAACCTCA | ACTCCCGCGA | CCAGCTGGAG | CGGGTGCTCT | TTGACGAGCT | GGGCCTGCCT | 1500 |
| 206 | GCCATCGGCA | AGACGGAGAA | GACGGGGAAA | CGCTCCACCA | GCGCTGCCGT | GCTGGAGGCC | 1560 |
| 208 | CTGCGAGAGG | CCCACCCAT | CGTGGACCGC | ATCCTGCAGT | ACCAGGAGCT | CACCAAGCTC | 1620 |
| 210 | AAGAACACCT | ACATAGACCC | CCTGCCCGCC | CTGGTCCACC | CCAAGACCCG | CGGCTCCAC | 1680 |
| 212 | ACCCGTTCA | ACCAGACGGC | CACGCCACG | GGCAGGCTTT | CCAGCTCCGA | CCCCAACCTG | 1740 |
| 214 | CAGAACATCC | CCGTGCGCAC | CCCTCTGGC | CAGGCATCC | GCCGAGCCTT | CGTGGCCGAG | 1800 |
| 216 | GAGGGCTGGG | TGCTGGTGGT | CTTGGACTAC | AGCCAGATTG | AGCTTCGGGT | CCTGGCCAC | 1860 |
| 218 | CTCTCCGGGG | ACGAGAACCT | GATCCGGGTC | TTTCAGGAGG | GGAGGGACAT | CCACACCCAG | 1920 |
| 220 | ACCGCCAGCT | GGATGTTCGG | CGTTTCCCCC | GAAGGGTAG | ACCCCTGTGAT | GGCCCGGGCG | 1980 |
| 222 | GCCAAGACCA | TCAACTTCGG | GGTGTCTAC | GGCATGTCCG | CCCACCGCCT | CTCCGGGGAG | 2040 |
| 224 | CTTCCATCC | CCTACGAGGA | GGCGGTGGCC | TTCATTGAGC | GCTACTTCCA | GAGCTACCC | 2100 |
| 226 | AAGGTGGGGG | CCTGGATTGA | GGGGACCCCTC | GAGGAGGGCC | GCCGGCGGGG | GTATGTGGAG | 2160 |
| 228 | ACCCCTTCG | GCCGCCGGCG | CTATGTGCC | GACCTAACG | CCCGGGTGAA | GAGCGTGCAC | 2220 |
| 230 | GAGGCGGGCG | AGCGCATGGC | CTTCAACATG | CCGGTCCAGG | GCACCGCCGC | CGACCTCATG | 2280 |
| 232 | AAGCTGGCCA | TGGTGGGCT | TTTCCCCCGG | CTTCAGGAAC | TGGGGGCGAG | GATGCTTTG | 2340 |
| 234 | CAGGTGCACG | ACGAGCTGGT | CCTCGAGGCC | CCCAAGGACC | GGGCGGAGAG | GGTAGCCGCT | 2400 |
| 236 | TTGGCCAAGG | AGGTCAATGGA | GGGGGTCTGG | CCCCTGCAGG | TGCCCCTGGA | GGTGGAGGTG | 2460 |
| 238 | GGCCTGGGGG | AGGACTGGCT | CTCCGCCAAG | GAGTAG | | | 2496 |
| 240 | (2) INFORMATION FOR SEQ ID NO: 3: | | | | | | |
| 242 | (i) SEQUENCE CHARACTERISTICS: | | | | | | |
| 243 | (A) LENGTH: 2504 base pairs | | | | | | |
| 244 | (B) TYPE: nucleic acid | | | | | | |
| 245 | (C) STRANDEDNESS: double | | | | | | |
| 246 | (D) TOPOLOGY: linear | | | | | | |
| 248 | (ii) MOLECULE TYPE: DNA (genomic) | | | | | | |
| 252 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: | | | | | | |
| 254 | ATGGAGGCCGA | TGCTTCCGCT | CTTTGAACCC | AAAGGCCGGG | TCCTCCTGGT | GGACGGCCAC | 60 |
| 256 | CACCTGGCCT | ACCGCACCTT | CTTCGCCCTG | AAGGGCCTCA | CCACGAGCCG | GGGCGAACCG | 120 |

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/941,193A

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|-----|----------|---------------|------------------|----------|-------|--------|--------|----------|--------|--------|-----------|--------|----------|----------|---------|------|------|------|
| 258 | GTGCAGGC | GG | TCTACGG | CT | CC | CTCA | CC | CTGAAG | GGACGG | TAC | 180 | | | | | | | |
| 260 | AAGGCC | TCT | TCGTGG | TT | TGACG | CCAG | GCCC | CTCCT | TCCGCC | ACGA | GGCCTACG | 240 | | | | | | |
| 262 | GCC | TACA | AGG | CGGGGAGG | GC | CCGAC | CCC | GAGGACTT | CGCC | GCAG | TAC | 300 | | | | | | |
| 264 | AAGGAG | CTGG | TGGAC | CTCCT | GGGG | TTT | AACC | CGAGG | TCCC | CGGCTA | CGAGGCGG | 360 | | | | | | |
| 266 | GACG | TCTCG | CCAC | CCCTGG | CAAGA | AGGCG | GAAA | AGGAGG | GGTAC | CGAGG | TACGAGGT | 420 | | | | | | |
| 268 | ACCGCC | GACC | GAC | CTCTA | CCA | ACTCG | TCCG | ACCG | TCGCC | GTCTC | TCT | 480 | | | | | | |
| 270 | GCCC | AC | CCTCA | TCAC | CCC | GGGA | GTGG | GCTT | GGAGA | GTACG | GCAGGCC | 540 | | | | | | |
| 272 | GTGG | ACTT | CC | CGCC | CTCG | GGGG | GACCCC | TCCG | ACAACC | TCCC | CGGGGT | 600 | | | | | | |
| 274 | GGGG | GAGA | AGA | CCG | CCCT | CAA | GCTC | CTCAAG | GAGT | GGGGAA | GCCTG | 660 | | | | | | |
| 276 | AACT | TGG | GACC | GGGT | AAAG | AGCC | AGAAA | ACGTC | CGGG | GAGAAG | TCAAGGCCA | 720 | | | | | | |
| 278 | CTC | AGG | GCT | C | CTT | GGAG | CT | CCC | GGGT | CGCAC | TCCC | CTGGA | 780 | | | | | |
| 280 | GCCC | AGGG | GG | GGGAG | CCC | GGAGGG | CTT | AGGG | CCT | GGAGAG | GCT | GGAGTT | 840 | | | | | |
| 282 | GGC | AGC | CCT | TCC | ACG | AGT | CCG | GGG | CTC | CTG | GGAGG | CCCC | 900 | | | | | |
| 284 | TGG | CCCC | CGC | CGGA | AGGG | GGC | CTCG | GGGG | TTCG | CTCT | CCC | GCCCCG | 960 | | | | | |
| 286 | GCGG | GAG | CTT | TA | AGC | CC | CTG | CAGG | GAC | GGCC | GCGG | TGCA | CCGG | 1020 | | | | |
| 288 | TTGG | C | GGGG | GC | TAA | AGG | AC | CT | CAAG | GG | TCG | CCG | TCTC | 1080 | | | | |
| 290 | TTGG | C | CTCG | GA | GGG | AGGG | GCT | CT | CTCAAG | GG | CC | CT | TAC | 1140 | | | | |
| 292 | CTC | CTGG | A | CC | TCAAC | ACAC | CAC | CCCC | GAG | GGG | TGG | CCG | GCG | 1200 | | | | |
| 294 | ACGG | AGG | GAC | CC | GCCC | CACCG | GGC | CC | CTCG | AGG | TGGAG | AC | CTCTTAAG | 1260 | | | | |
| 296 | CGC | CTCG | GAG | GGG | AGG | GAGA | GCT | CTT | GGAG | AGG | TGG | AGG | AA | 1320 | | | | |
| 298 | CGGG | TCTG | GG | CCCAC | ATG | GGGA | GGCC | ACCG | GTAC | GGCTG | ACGT | GGCC | TA | 1380 | | | | |
| 300 | CTT | CC | CTG | GG | AGCT | TGCG | GA | GAT | CCG | CCTG | AGG | AGGT | CTT | CGCTTGCG | 1440 | | | |
| 302 | GGCC | AC | CC | CT | CA | CT | CC | GGG | AC | GTG | AAA | GGGT | GCT | CTT | TGACGAG | 1500 | | |
| 304 | AGG | CT | CC | CG | CTT | GGG | AA | GAC | GCAA | AG | AC | AGG | CA | GC | 1560 | | | |
| 306 | CTG | GAG | GG | CC | AC | CC | ATC | CC | AC | TG | GAGA | AGA | TCC | CAG | 1620 | | | |
| 308 | ACCA | AG | GCT | CA | AG | AC | CTA | CG | AC | CT | CC | AG | GG | AC | GGG | 1680 | | |
| 310 | CGC | CT | CC | A | CC | CG | CT | CC | AC | GG | CC | AC | GG | GT | CCG | 1740 | | |
| 312 | CCCA | AC | CT | GC | AGA | AC | AT | CCC | CG | CC | CT | GGG | CC | CT | TC | 1800 | | |
| 314 | GTGG | CC | GAG | GG | GGG | TG | GG | GG | CT | GG | ACT | TATA | GCA | GAT | AGA | 1860 | | |
| 316 | CTC | GCC | C | AC | TCT | GGG | GA | AAA | AC | CTG | GGT | CT | TCC | AGG | AGGG | 1920 | | |
| 318 | CA | AC | CC | A | CG | CA | AG | CTG | TG | G | TG | CCCC | CCG | GG | AGG | CT | 1980 | |
| 320 | CGC | GGG | CG | GG | CA | AG | AC | GG | TG | GG | CT | CT | AC | G | GT | CC | 2040 | |
| 322 | TCC | CAG | G | GG | CC | AT | CCC | CTG | GG | GG | CT | GG | CC | CT | GG | CT | 2100 | |
| 324 | GCT | CCC | CC | AA | GG | TG | GA | AGA | AG | CC | CTG | GA | GG | GGG | GG | G | 2160 | |
| 326 | AC | GTG | GG | AA | AC | C | C | GG | TG | GG | CT | AC | GC | TA | AC | GG | 2220 | |
| 328 | GCG | T | CAG | GG | GG | CA | GG | CG | GT | CC | AG | GG | GC | AC | CG | CC | 2280 | |
| 330 | AC | CT | CAT | G | G | TG | CC | GC | AT | GG | CT | GG | CC | GT | GG | GC | 2340 | |
| 332 | TG | C | CT | CCA | GG | TG | CC | AC | G | AG | CT | GG | CC | GG | CC | GG | 2400 | |
| 334 | TGG | GGG | CTT | GG | CC | AA | GG | GA | GG | CC | TAT | CC | CTG | CC | GT | GG | AGG | 2460 |
| 336 | TGG | AGG | TG | GG | G | AT | GG | CTT | CC | GG | CA | AG | GG | TT | AG | GT | 2504 | |
| 338 | (2) | INFORMATION | FOR | SEQ | ID | NO: | 4: | | | | | | | | | | | |
| 340 | (i) | SEQUENCE | CHARACTERISTICS: | | | | | | | | | | | | | | | |
| 341 | (A) | LENGTH: | 832 | amino | acids | | | | | | | | | | | | | |
| 342 | (B) | TYPE: | amino | acid | | | | | | | | | | | | | | |
| 343 | (C) | STRANDEDNESS: | single | | | | | | | | | | | | | | | |
| 344 | (D) | TOPOLOGY: | linear | | | | | | | | | | | | | | | |
| 346 | (ii) | MOLECULE | TYPE: | protein | | | | | | | | | | | | | | |
| 350 | (xi) | SEQUENCE | DESCRIPTION: | SEQ | ID | NO: | 4: | | | | | | | | | | | |
| 352 | Met | Arg | Gly | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | Leu | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 353 | 1 | 5 | 10 | 15 | | | | | | | | | | | | |
| 355 | Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | His | Ala | Leu | Lys | Gly |
| 356 | | | | | | 20 | | | | 25 | | | | | 30 | |
| 358 | Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | Ala |
| 359 | | | | | | 35 | | | | 40 | | | | | 45 | |
| 361 | Lys | Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Ala | Val | Ile | Val |
| 362 | | | | | | 50 | | | | 55 | | | | | 60 | |
| 364 | Val | Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Gly | Gly |
| 365 | | | | | | 65 | | | | 70 | | | | | 80 | |
| 367 | Tyr | Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | Leu |
| 368 | | | | | | 85 | | | | 90 | | | | | 95 | |
| 370 | Ala | Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Ala | Arg | Leu | Glu |
| 371 | | | | | | 100 | | | | 105 | | | | | 110 | |
| 373 | Val | Pro | Gly | Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Ser | Leu | Ala | Lys | Lys |
| 374 | | | | | | 115 | | | | 120 | | | | | 125 | |
| 376 | Ala | Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Lys | Asp |
| 377 | | | | | | 130 | | | | 135 | | | | | 140 | |
| 379 | Leu | Tyr | Gln | Leu | Leu | Ser | Asp | Arg | Ile | His | Val | Leu | His | Pro | Glu | Gly |
| 380 | | | | | | 145 | | | | 150 | | | | | 160 | |
| 382 | Tyr | Leu | Ile | Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | Pro |
| 383 | | | | | | 165 | | | | 170 | | | | | 175 | |
| 385 | Asp | Gln | Trp | Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp | Asn |
| 386 | | | | | | 180 | | | | 185 | | | | | 190 | |
| 388 | Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | Leu |
| 389 | | | | | | 195 | | | | 200 | | | | | 205 | |
| 391 | Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | Leu |
| 392 | | | | | | 210 | | | | 215 | | | | | 220 | |
| 394 | Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | Lys |
| 395 | | | | | | 225 | | | | 230 | | | | | 240 | |
| 397 | Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | Val |
| 398 | | | | | | 245 | | | | 250 | | | | | 255 | |
| 400 | Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | Phe |
| 401 | | | | | | 260 | | | | 265 | | | | | 270 | |
| 403 | Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | Leu |
| 404 | | | | | | 275 | | | | 280 | | | | | 285 | |
| 406 | Glu | Ser | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | Gly |
| 407 | | | | | | 290 | | | | 295 | | | | | 300 | |
| 409 | Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Lys | Glu | Pro | Met | Trp | Ala | Asp |
| 410 | | | | | | 305 | | | | 310 | | | | | 320 | |
| 412 | Leu | Leu | Ala | Leu | Ala | Ala | Ala | Arg | Gly | Gly | Arg | Val | His | Arg | Ala | Pro |
| 413 | | | | | | 325 | | | | 330 | | | | | 335 | |
| 415 | Glu | Pro | Tyr | Lys | Ala | Leu | Arg | Asp | Leu | Lys | Glu | Ala | Arg | Gly | Leu | Leu |
| 416 | | | | | | 340 | | | | 345 | | | | | 350 | |
| 418 | Ala | Lys | Asp | Leu | Ser | Val | Leu | Ala | Leu | Arg | Glu | Gly | Leu | Gly | Leu | Pro |
| 419 | | | | | | 355 | | | | 360 | | | | | 365 | |
| 421 | Pro | Gly | Asp | Asp | Pro | Met | Leu | Leu | Ala | Tyr | Leu | Leu | Asp | Pro | Ser | Asn |
| 422 | | | | | | 370 | | | | 375 | | | | | 380 | |
| 424 | Thr | Thr | Pro | Glu | Gly | Val | Ala | Arg | Arg | Tyr | Gly | Gly | Glu | Trp | Thr | Glu |
| 425 | | | | | | 385 | | | | 390 | | | | | 400 | |

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/23/2002
PATENT APPLICATION: US/09/941,193A TIME: 13:04:52

Input Set : A:\Seqsub2.app
Output Set: N:\CRF3\07232002\I941193A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396
Seq#:8; Xaa Pos. 2,63,109,186,205,209,227,228,233,240,243,244,247,260,290
Seq#:8; Xaa Pos. 329,336,340,368,414,417,418,431,551,605,773,794,798,823,833

VERIFICATION SUMMARY

DATE: 07/23/2002

PATENT APPLICATION: US/09/941,193A

TIME: 13:04:52

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\07232002\I941193A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192
L:1165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:288
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832